RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09185781B

Source: ICW16

Date Processed by STIC: 3/1/05

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IFW16

RAW SEQUENCE LISTING   DATE: 03/01/2005
PATENT APPLICATION: US/09/857,581B   TIME: 15:18:42

Input Set : **A:\BB1339 RCE Seq Lst.txt**
Output Set: **N:\CRF4\03012005\I857581B.raw**

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 3 <110> APPLICANT: Fader, Gary M.
 4        Jung, Woosuk
 5        Brian, McGonigle
 6        Odell, Joan T.
 7        Yu, Xiaodan
 9 <120> TITLE OF INVENTION: Nucleic Acid Fragments Encoding Isoflavone Synthase
11 <130> FILE REFERENCE: BB1339RCE
13 <140> CURRENT APPLICATION NUMBER: US/09/857,581B
14 <141> CURRENT FILING DATE: 2001-06-05
16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01,772
17 <151> PRIOR FILING DATE: 2000-01-26
19 <150> PRIOR APPLICATION NUMBER: 60/117,769
20 <151> PRIOR FILING DATE: 1999-01-27
22 <150> PRIOR APPLICATION NUMBER: 60/144,783
23 <151> PRIOR FILING DATE: 1990-07-20
25 <150> PRIOR APPLICATION NUMBER: 60/156,094
26 <151> PRIOR FILING DATE: 1999-09-24
28 <160> NUMBER OF SEQ ID NOS: 66
30 <170> SOFTWARE: PatentIn version 3.3
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33 <211> LENGTH: 1756
34 <212> TYPE: DNA
35 <213> ORGANISM: Glycine max
37 <400> SEQUENCE: 1
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39 ttcacgatgt tgctggaact tgcacttggt ttgtttgtgt tagctttgtt tctgcacttg     120
40 cgtcccacac caagtgcaaa atcaaaagca cttcgccacc tcccaaaccc tccaagccca     180
41 aagcctcgtc ttcccttcat tggccacctt cacctcttaa aagataaact tctccactat     240
42 gcactcatcg atctctccaa aaagcatggc cccttattct ctctctcctt cggctccatg     300
43 ccaaccgtcg ttgcctccac ccctgagttg ttcaagctct tcctccaaac ccacgaggca     360
44 acttccttca acacaaggtt ccaaacctct gccataagac gcctcactta cgacaactct     420
45 gtggccatgg ttccattcgg accttactgg aagttcgtga ggaagctcat catgaacgac     480
46 cttctcaacg ccaccaccgt caacaagctc aggcctttga ggacccaaca gatccgcaag     540
47 ttccttaggg ttatggccca aagcgcagag gcccagaagc cccttgacgt caccgaggag     600
48 cttctcaaat ggaccaacag caccatctcc atgatgatgc tcggcgaggc tgaggagatc     660
49 agagacatcg ctcgcgaggt tcttaagatc ttcggcgaat acagcctcac tgacttcatc     720
50 tggccttttga agtatctcaa ggttggaaag tatgagaaga ggattgatga catcttgaac     780
51 aagttcgacc ctgtcgttga aagggtcatc aagaagcgcc gtgagatcgt cagaaggaga     840
52 aagaacggag aagttgttga gggcgaggcc agcggcgtct tcctcgacac tttgcttgaa     900
53 ttcgctgagg acgagaccat ggagatcaaa attaccaagg agcaaatcaa gggccttgtt     960
54 gtcgactttt tctctgcagg gacagattcc acagcggtgg caacagagtg ggcattggca    1020
55 gagctcatca acaatcccag ggtgttgcaa aaggctcgtg aggaggtcta cagtgttgtg    1080
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59 caagtaggaa gggaccccaa atactgggac agaccatcag aattccgtcc cgagaggttc      1320
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61 ctcctcccat ttgggtctgg gaggagaatg tgccctggtg tcaatttggc tacttcagga      1440
62 atggcaacac ttcttgcatc tcttatccaa tgctttgacc tgcaagtgct gggccctcaa      1500
63 ggacaaatat tgaaaggtga tgatgccaaa gttagcatgg aagagagagc tggcctcaca      1560
64 gttccaaggg cacatagtct cgtttgtgtt ccacttgcaa ggatcggcgt tgcatctaaa      1620
65 ctcctttctt aattaagata atcatcatat acaatagtag tgtcttgcca tcgcagttgc      1680
66 tttttatgta ttcataatca tcatttcaat aaggtgtgac tggtacttaa tcaagtaatt      1740
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79              20                  25                  30
81 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
82          35                  40                  45
84 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
85      50                  55                  60
87 Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met Pro Thr
88 65              70                  75                  80
90 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
91              85                  90                  95
93 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
94              100                 105                 110
96 Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
97          115                 120                 125
99 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
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102 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
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105 Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp Val Thr
106                 165                 170                 175
108 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
109             180                 185                 190
111 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
112         195                 200                 205
114 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Tyr Leu
115     210                 215                 220
117 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
118 225                 230                 235                 240
120 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
121                 245                 250                 255
123 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly Val Phe
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Input Set : A:\BB1339 RCE Seq Lst.txt
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126 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
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129 Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
130     290              295              300
132 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
133 305              310              315              320
135 Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val Tyr Ser
136             325              330              335
138 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
139         340              345              350
141 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
142     355              360              365
144 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
145     370              375              380
147 Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp Gln Val
148 385              390              395              400
150 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
151             405              410              415
153 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
154         420              425              430
156 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
157         435              440              445
159 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
160     450              455              460
162 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
163 465              470              475              480
165 Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
166             485              490              495
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175 <211> LENGTH: 27
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179 <220> FEATURE:
180 <223> OTHER INFORMATION: Oligonucleotide primer used in construction of WHT1
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186 <211> LENGTH: 32
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188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Oligonucleotide primer used in construction of yeast strain
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193 <400> SEQUENCE: 4
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202 <223> OTHER INFORMATION: Oligonucleotide primer
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230 <211> LENGTH: 27
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234 <220> FEATURE:
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243 <213> ORGANISM: Glycine max
245 <400> SEQUENCE: 9
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247 ttgaacttgc acttggttta ttggttttgg ctctgtttct gcacttgcgt cccacaccca  120
248 ctgcaaaatc aaaagcactt cgccatctcc caaacccacc aagcccaaag cctcgtcttc  180
249 ccttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc  240
250 tctccaaaaa acatggtccc ttattctctc tctactttgg ctccatgcca accgttgttg  300
251 cctccacacc agaattgttc aagctcttcc tccaaacgca cgaggcaact tccttcaaca  360
252 caaggttcca aacctcagcc ataagacgcc tcacctatga tagctcagtg gccatggttc  420
253 ccttcggacc ttactggaag ttcgtgagga agctcatcat gaacgacctt cccaacgcca  480
254 ccactgtaaa caagttgagg cctttgagga cccaacagac ccgcaagttc cttagggtta  540
255 tggcccaagg cgcagaggca cagaagcccc ttgacttgac cgaggagctt ctgaaatgga  600
256 ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc  660
257 gcgaggttct taagatcttt ggcgaataca gcctcactga cttcatctgg ccattgaagc  720
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260 ttgttgaggg tgaggtcagc ggggttttcc ttgacacttt gcttgaattc gctgaggatg   900
261 agaccatgga gatcaaaatc accaaggacc acatcgaggg tcttgttgtc gactttttct   960
262 cggcaggaac agactccaca gcggtggcaa cagagtgggc attggcagaa ctcatcaaca  1020
263 atcctaaggt gttggaaaag gctcgtgagg aggtctacag tgttgtggga aaggacagac  1080
264 ttgtggacga agttgacact caaaaccttc cttacattag agcaatcgtg aaggagacat  1140
265 tccgcatgca cccgccactc ccagtggtca aaagaaagtg cacagaagag tgtgagatta  1200
266 atggatatgt gatcccagag ggagcattga ttctcttcaa tgtatggcaa gtaggaagag  1260
267 accccaaata ctgggacaga ccatcggagt tccgtcctga gaggttccta gagacagggg  1320
268 ctgaagggga agcagggcct cttgatctta ggggacaaca ttttcaactt ctcccatttg  1380
269 ggtctgggag gagaatgtgc cctggagtca atctggctac ttcgggaatg gcaacacttc  1440
270 ttgcatctct tattcagtgc ttcgacttgc aagtgctggg tccacaagga cagatattga  1500
271 agggtggtga cgccaaagtt agcatggaag agagagccgg cctcactgtt ccaagggcac  1560
272 atagtcttgt ctgtgttcca cttgcaagga tcggcgttgc atctaaactc ctttcttaat  1620
273 taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa  1680
274 ggtctcgttc atctactttt tatgaagtat ataagccctt ccatgcacat tgtatcatct  1740
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276 actataaact atcaatcctt atat                                         1824
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279 <211> LENGTH: 521
280 <212> TYPE: PRT
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288             20                  25                  30
290 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
291         35                  40                  45
293 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
294     50                  55                  60
296 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
297 65                  70                  75                  80
299 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
300                 85                  90                  95
302 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
303             100                 105                 110
305 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
306             115                 120                 125
308 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr
309     130                 135                 140
311 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
312 145                 150                 155                 160
314 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
315                 165                 170                 175
317 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
318             180                 185                 190
320 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/01/2005
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Input Set : A:\BB1339 RCE Seq Lst.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:66; Xaa Pos. 122,124,129,140,147,159,162,166,170,175,183,187,191,209
Seq#:66; Xaa Pos. 219,223,253,259,263,264,268,272,285,292,293,295,301,306
Seq#:66; Xaa Pos. 311,312,325,328,329,334,342,377,381,385,387,393,394,402
Seq#:66; Xaa Pos. 404,413,422,428,429,435,447,453,459,485

VERIFICATION SUMMARY   DATE: 03/01/2005
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Input Set : **A:\BB1339 RCE Seq Lst.txt**
Output Set: **N:\CRF4\03012005\I857581B.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
M:341 Repeated in SeqNo=66